



NOAA Technical Memorandum NMFS-AFSC-232

# **Genetic Stock Composition Analysis of Chinook Salmon Bycatch Samples from the 2010 Bering Sea Trawl Fisheries**

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C. M. Guthrie, III, H. T. Nguyen, and J. R. Guyon

**U.S. DEPARTMENT OF COMMERCE**  
National Oceanic and Atmospheric Administration  
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## ABSTRACT

A genetic analysis of samples from the Chinook salmon (*Oncorhynchus tshawytscha*) bycatch of the 2010 Bering Sea groundfish trawl fishery was undertaken to determine the overall stock composition of the sample set. Samples were genotyped for 43 single nucleotide polymorphism DNA markers and results were estimated using the Alaska Department of Fish and Game (ADF&G) SNP baseline. In 2010, genetic samples were collected as part of the observer's species-composition analysis. This sampling change for 2010 was an interim measure implemented until recommended systematic sampling protocols could be finalized. Consequently, stock composition estimates apply to the sample set and may not represent the entire Chinook salmon bycatch. Based on the analysis of 826 Chinook salmon bycatch samples collected throughout the 2010 Bering Sea trawl fishery, Coastal Western Alaska stocks dominated the sample set (42%), with smaller contributions from Upper Yukon River (20%), North Alaska Peninsula (14%) and Middle Yukon River (11%) stocks. The annual estimates for the 2010 Chinook salmon bycatch sample set were generally similar to the 2005–2009 Chinook salmon bycatch estimates, although there were higher proportions of Yukon River stocks and lower proportions of Coastal Western Alaska stocks in 2010. Analysis of temporal groupings within the groundfish “A” and “B” seasons revealed changes in stock composition during the course of the year with lower contribution of North Alaska Peninsula and Yukon River stocks and higher concentrations of Pacific Northwest and British Columbia stocks during the “B” season, but leaves unanswered whether these changes are due to temporal or spatial differences in the sample set.



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## INTRODUCTION

The Bering Sea is a known feeding habitat for multiple brood years of Chinook salmon (*Oncorhynchus tshawytscha*) from many different localities in North America and Asia. Determining the geographic origin and stock composition of salmon caught in federally managed fisheries is essential to understanding whether fisheries management could address conservation concerns. This report provides genetic stock identification results for a set of Chinook salmon bycatch samples collected from the U.S. Bering Sea groundfish trawl fisheries. National Marine Fisheries Service (NMFS) geographical statistical areas associated with the groundfish fishery are shown in Figure 1 and are used later in the report to describe the spatial distribution of the Chinook salmon bycatch and genetic samples.

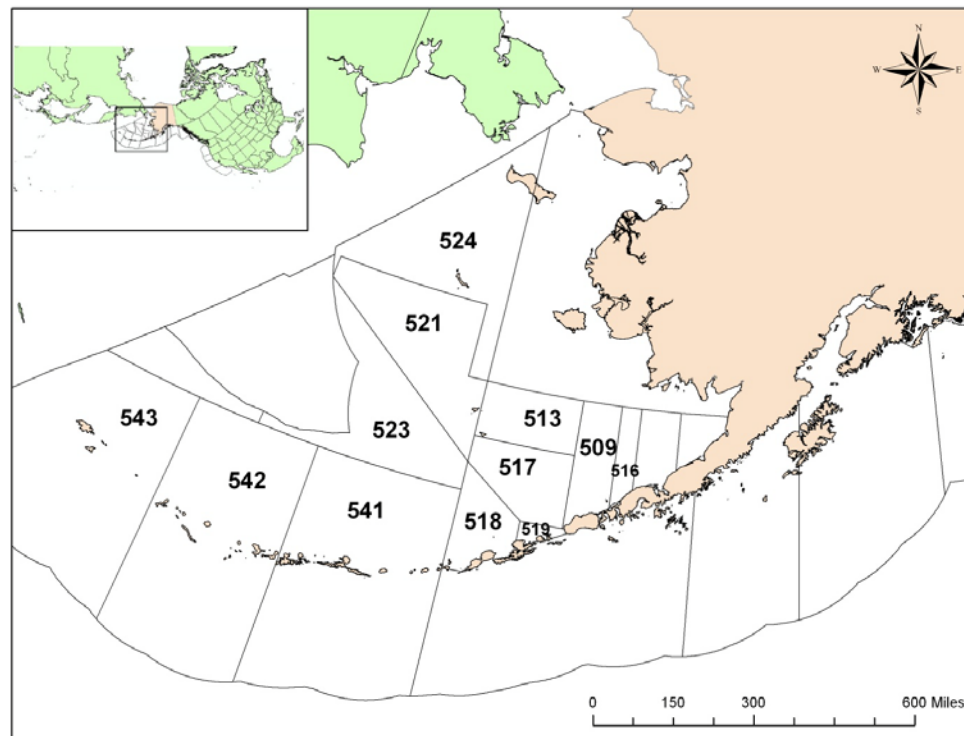


Figure 1. -- NMFS statistical areas associated with the Bering Sea Aleutian Island (BSAI) trawl fishery.

The goal of this report is to present stock composition estimates for samples collected from the bycatch of the Bering Sea trawl fishery, but it is important to understand the limitations for making accurate estimates of the entire bycatch imposed by the sampling distribution and the genetic baseline. This report is divided into the following five sections: Introduction, Sample Distribution, Genetic Stock Composition, Comparison with Previous Estimates, and a Summary. The analysis uses a single nucleotide polymorphism (SNP) baseline provided by the Alaska Department of Fish and Game (ADF&G) (Templin et al. 2011) and was used previously to estimate stock composition of samples from the 2005, 2006, 2007, 2008, and 2009 Chinook salmon bycatch (Guyon et al. 2010a and b; NMFS 2009). For additional information regarding background and methodology, this report is intended to be supplemented with the Chinook salmon bycatch report prepared previously for the 2008 Bering Sea trawl fishery (Guyon et al. 2010a).

## SAMPLE DISTRIBUTION

Samples were collected by the Alaska Fisheries Science Center's (AFSC) North Pacific Observer Program as a Special Project (designated "Salmon Genetic Project") for the Auke Bay Laboratories (ABL). Samples of axillary process tissue for genetic analysis were collected as part of the species composition analysis throughout the 2010 groundfish "A" and "B" seasons. Axillary process tissue was stored in coin envelopes which were labeled, frozen, and shipped to ABL. While the majority of the Chinook salmon bycatch genetic samples were derived from the bottom and mid-water pollock trawl fishery (78% pollock, 7% cod, and 15% unknown), the actual target was only determined after the season was completed as the most common catch in the haul or offload. In addition, a vessel can theoretically participate in various fisheries on a particular cruise before an offload. For these reasons, stock composition estimates are provided

for the entire data set and presented as the stock composition of the BSAI groundfish trawl fishery for 2010.

In 2010, an estimated 12,532 Chinook salmon were taken in the bycatch of the Bering Sea groundfish trawl fisheries (NMFS 2011), of which 9,513 were estimated from the trawl “A” season and 3,019 were estimated for the “B” season. The majority of Chinook salmon were taken as bycatch of the Bering Sea pollock fishery (9,737 in 2010). The year with the highest overall Chinook bycatch in the Bering Sea was 2007 (Fig. 2) when an estimated 129,567 were taken. The genetic sample set for the 2010 “A” season Chinook salmon bycatch was 702 fish, corresponding to a sampling rate of 7.4%. The genetic sample set for the 2010 “B” season Chinook bycatch was 124 fish, corresponding to a sampling rate of 4.1%. The annual sampling rate for the entire year was 6.6%.

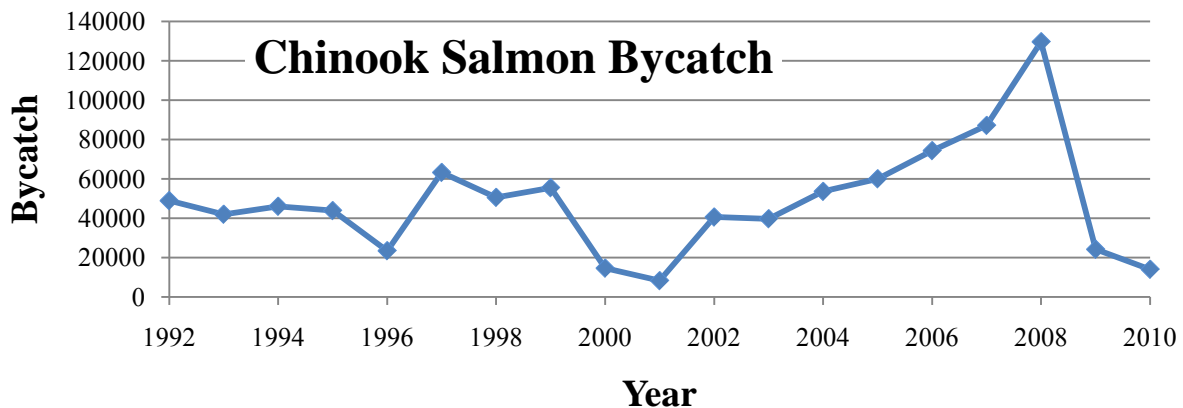


Figure 2. -- Yearly estimates for the Chinook salmon bycatch from the Bering Sea trawl fishery (NMFS 2011).

Potential biases associated with the collection of genetic samples from the bycatch are well documented, and have the potential to affect resulting stock composition estimates (Pella and Geiger 2009). Potential spatial and temporal biases associated with the 2010 Chinook salmon bycatch sample sets were evaluated by comparing the genetic sample distribution with

the overall bycatch estimate distribution (Fig. 3). During 2010, the overall bycatch and genetic samples were generally comparable in their temporal distribution.

To evaluate the sample spatial distribution, the Chinook salmon bycatch was compared with the bycatch samples by statistical area over time (Fig. 4). Spatial and temporal sample biases can become more apparent at these higher resolution scales. For samples collected from offloads in which the vessel fished in multiple areas, the sample location of the entire catch of a fishing trip was identified as the location of the first haul, although generally those areas were in close proximity to each other. Overall, the sampling of the Chinook salmon bycatch in the 2010 Bering Sea trawl fishery was in proportion to the catch, although the “B” season sample size was slightly underrepresented (Fig. 4). The sample spatial and temporal distribution was improved in 2010 compared to previous years when samples were collected more opportunistically (Guyon et al. 2010a, 2010b). In 2010, genetic samples were collected as part of the observer’s species composition analysis. This sampling change for 2010 was an interim measure implemented until systematic sampling protocols recommended by Pella and Geiger (2009) could be finalized.

#### GENETIC STOCK COMPOSITION

DNA was extracted from axillary process tissue and matrix-assisted laser desorption/ionization - time of flight (MALDI-TOF) genotyping was performed as described previously (Guyon et al. 2010a) using a Sequenom MassARRAY iPLEX platform (Gabriel et al. 2009) to genotype 43 SNP DNA markers represented in the Chinook salmon baseline (Templin et al. 2011). The SNP baseline contains genetic information for 172 populations of Chinook salmon grouped into 11 geographic regions. This baseline was used previously for the genetic analysis of the 2005, 2006, 2007, 2008, and 2009 Bering Sea Chinook bycatch (NMFS 2009; Guyon et al. 2010a, b). In addition to internal MALDI-TOF chip controls, 10 previously

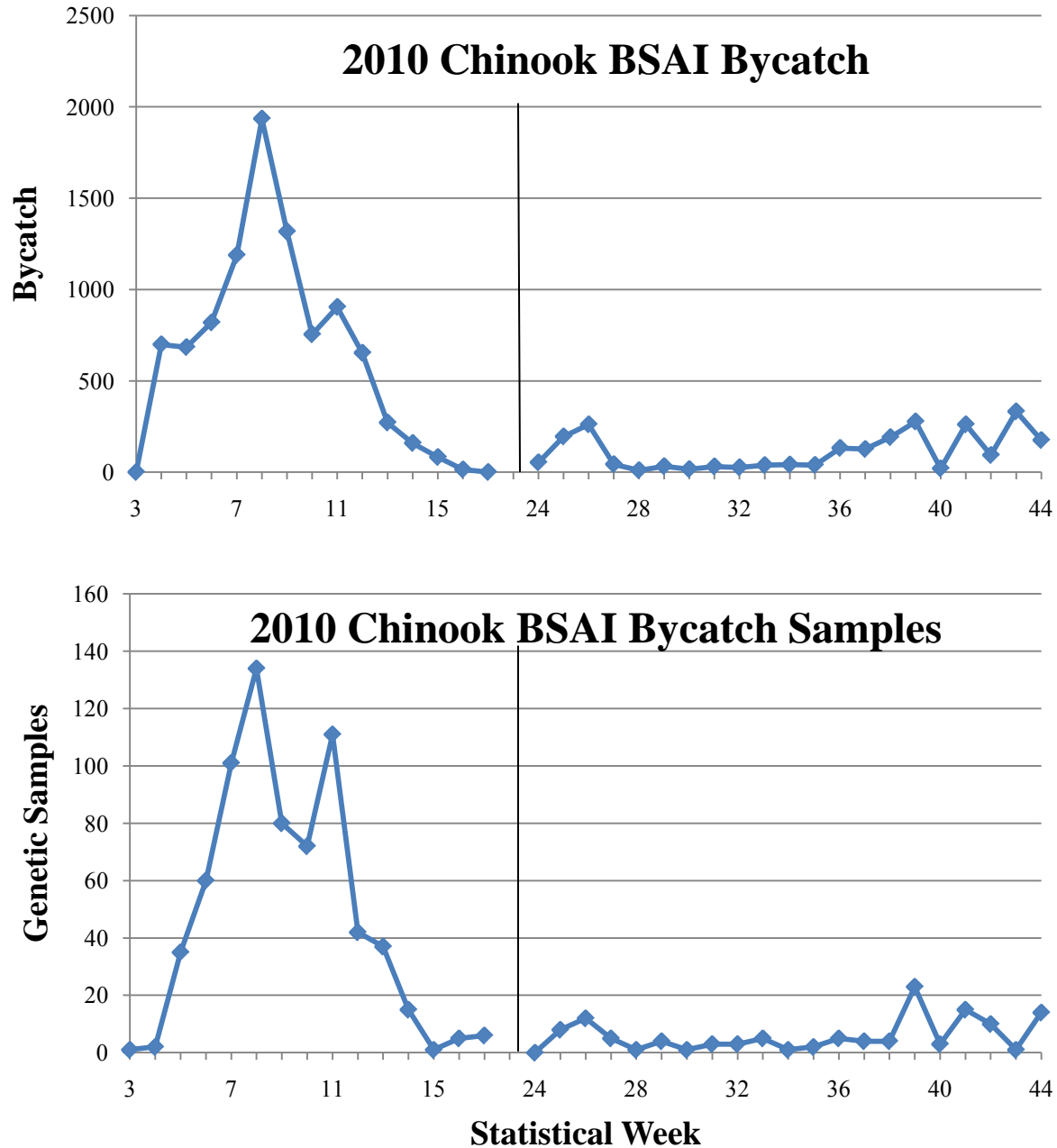


Figure 3.-- Number of Chinook salmon bycatch and genetic samples graphed by statistical week. Top panel: Distribution of all Chinook salmon caught in the 2010 Bering Sea groundfish trawl fishery. Bottom panel: Distribution of the available 826 genetic samples from the 2010 bycatch. Weeks 3-17 correspond to the groundfish “A” season, whereas weeks 24-44 correspond to the “B” season, the demarcation of which is a vertical line.

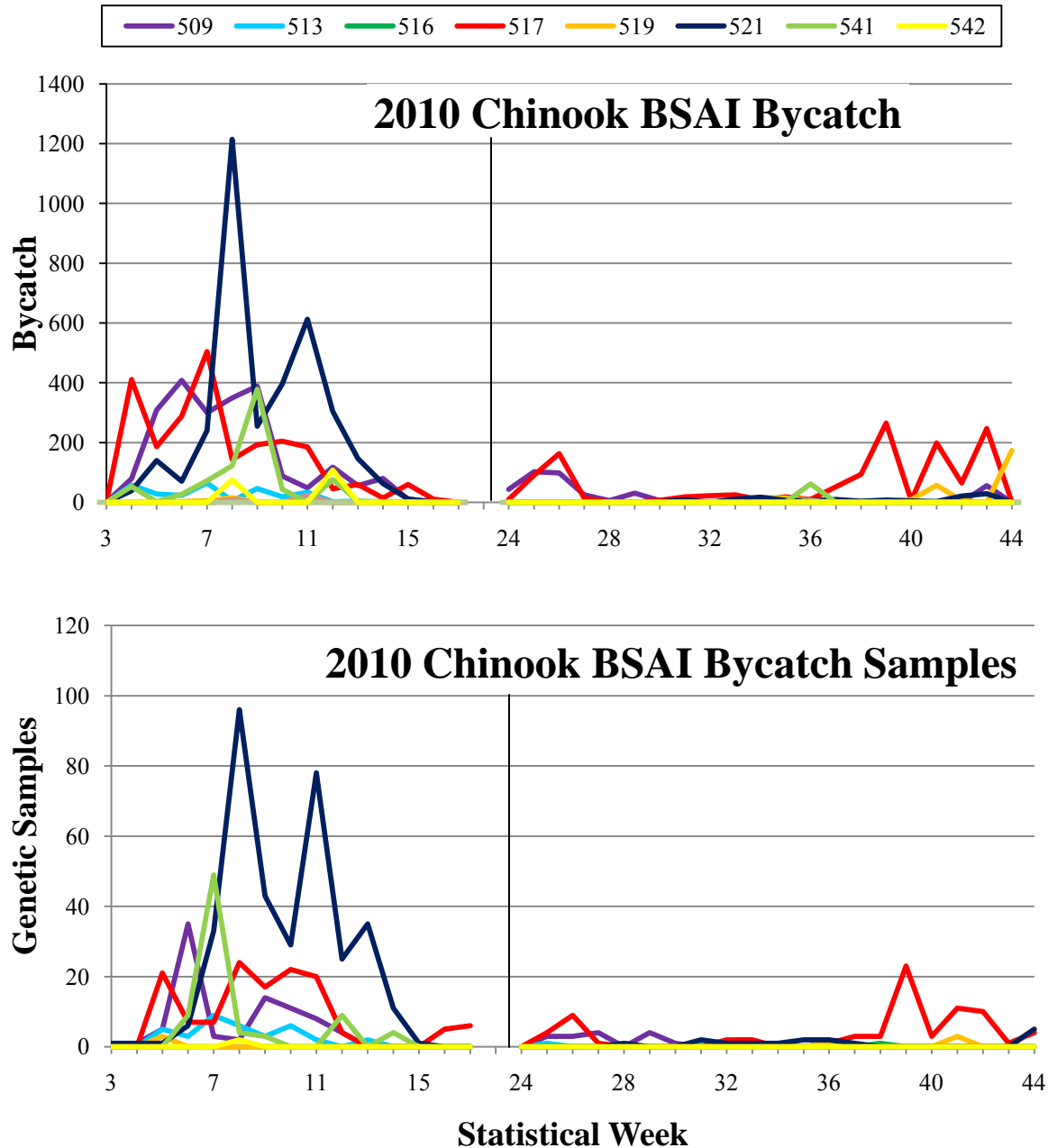


Figure 4. -- Comparison of the Chinook salmon bycatch by time and area with the distribution of available genetic samples. Top panel: Distribution of the estimated Chinook salmon caught in the 2010 BSAI groundfish trawl fishery. Not graphed were an estimated 33 fish from area 523, 5 from area 524, and 5 from area 543. Bottom panel: Distribution of the available 826 genetic samples from the 2010 bycatch. Not graphed were 1 fish from areas 516, and 524 each; 3 from area 523, and 4 from area 543. Weeks 3-17 correspond to the groundfish “A” season, whereas weeks 24-44 correspond to the “B” season, the demarcation of which is a vertical line.

genotyped samples were included on each chip during the analyses and resulting genotypes were compared to those from ADF&G, which used TaqMan chemistries (Applied Biosystems). Concordance rates of 99.9% between the two chemistries for the 2010 controls confirmed the utility and compatibility of both genotyping methods.

From the 2010 Chinook salmon bycatch, a total of 1,028 samples were analyzed of which 994 samples were successfully genotyped for 35 or more of the 43 SNP loci, a success rate of 96.7%. These genotypes were analyzed in GenAlEx (Peakall and Smouse 2006) for data integrity, resulting in the removal of 7 fish: 4 with duplicate genotypes and 3 fish without date information. Of the remaining 987, there were 826 which were determined to be from the Bering Sea (160 were from the Gulf of Alaska and because of the small sample set were not analyzed in this report). The remaining 826 Bering Sea samples had genetic information for an average of 42.75 of 43 markers. Stock composition estimates were derived using both SPAM (maximum likelihood analysis) and BAYES (Bayesian analysis) software and both methods yielded almost identical stock composition estimates (Tables 1-3).

BAYES software uses a Bayesian algorithm to produce stock composition estimates and can account for missing alleles in the baseline (Pella and Masuda 2001). In contrast, SPAM uses a conditional maximum likelihood approach in which the mixture genotypes are compared directly with the baseline (ADF&G 2003). Although Version 3.7b of the SPAM software allows Bayesian modeling of baseline allele frequencies, these options were not utilized for the stock composition analyses. Convergence of the SPAM estimates was monitored with the “Percent of Maximum” value which was determined to be 91.1 (“A” estimate), 90.2 (“B” estimate), and 90.8 (overall estimate), exceeding the 90% guaranteed percent achievement of the maximal likelihood. For each BAYES analysis, 11 Monte Carlo chains starting at disparate values of stock proportions were configured such that 95% of the stocks came from one designated region with

weights equally distributed among the stocks of that region. The remaining 5% was equally distributed among remaining stocks from all other regions. For all estimates, a flat prior of 0.005814 (calculated as  $1/172$ ) was used for all 172 baseline populations. The analyses were completed for a chain length of 10,000 with the first 5,000 deleted during the burn-in phase when determining overall stock compositions. Convergence of the chains to posterior distributions of stock proportions was determined with Gelman and Rubin shrink statistics, which were all 1.05 or less for all the estimates, conveying strong convergence to a single posterior distribution (Pella and Masuda 2001).

Results (BAYES) suggest that 94% of the 702 samples from the “A” season originated from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska stock contributing the most (41%), followed by the Upper Yukon (24%), North Alaska Peninsula (16%), and Middle Yukon (12%) (Table 1). For the “B” season, over 47% of the 124 samples originated from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska region contributing the most (42%). This was followed by British Columbia (22%) and the Western U.S. coast (19%) (Table 2).

For the entire year, an estimated 87% of the bycatch samples were estimated to be from Alaskan river systems flowing into the Bering Sea with the Coastal Western Alaska stock contributing the most (42%), trailed by the Upper Yukon (20%), North Alaska Peninsula (14%), and the Middle Yukon (11%) (Table 3). The “overall” and “A” season stock compositions were similar, which was anticipated given that 85% of the samples were from the “A” season. In 2010, 76% of the Bering Sea groundfish Chinook salmon bycatch was from the “A” season.



Table 1. -- Regional SPAM and BAYES stock composition estimates for the 702 Chinook salmon samples from the bycatch of the 2010 “A” season Bering Sea groundfish trawl fishery. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrapping resamplings of the mixture. The BAYES mean estimates are provided with standard deviations (SD), 95% credible intervals, and the median estimate.

<u>Region</u>	<u>SPAM</u>	<u>SD</u>	<u>BAYES</u>	<u>SD</u>	<u>0.025</u>	<u>Median</u>	<u>97.5%</u>
Russia	<b>0.021</b>	0.004	<b>0.022</b>	0.006	0.012	0.021	0.034
Coast W AK	<b>0.437</b>	0.017	<b>0.414</b>	0.024	0.369	0.414	0.463
Mid Yukon	<b>0.106</b>	0.006	<b>0.121</b>	0.020	0.080	0.121	0.159
Up Yukon	<b>0.241</b>	0.013	<b>0.239</b>	0.020	0.201	0.239	0.279
N AK Pen	<b>0.143</b>	0.008	<b>0.162</b>	0.017	0.130	0.162	0.197
NW GOA	<b>0.014</b>	0.001	<b>0.006</b>	0.006	0.000	0.003	0.022
Copper	<b>0.002</b>	0.001	<b>0.000</b>	0.001	0.000	0.000	0.003
NE GOA	<b>0.000</b>	0.000	<b>0.000</b>	0.002	0.000	0.000	0.005
Coast SE AK	<b>0.003</b>	0.000	<b>0.003</b>	0.003	0.000	0.002	0.009
BC	<b>0.027</b>	0.002	<b>0.029</b>	0.007	0.017	0.028	0.043
WA/OR/CA	<b>0.006</b>	0.000	<b>0.005</b>	0.003	0.001	0.004	0.011

Table 2. -- Regional SPAM and BAYES stock composition estimates for the 124 Chinook salmon samples from the bycatch of the 2010 “B” season Bering Sea groundfish trawl fishery. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrapping resamplings of the mixture. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate.

<u>Region</u>	<u>SPAM</u>	<u>SD</u>	<u>BAYES</u>	<u>SD</u>	<u>0.025</u>	<u>Median</u>	<u>97.5%</u>
Russia	<b>0.024</b>	0.011	<b>0.024</b>	0.014	0.005	0.022	0.058
Coast W AK	<b>0.384</b>	0.037	<b>0.422</b>	0.051	0.323	0.422	0.520
Mid Yukon	<b>0.025</b>	0.009	<b>0.022</b>	0.022	0.000	0.017	0.078
Up Yukon	<b>0.005</b>	0.000	<b>0.001</b>	0.004	0.000	0.000	0.011
N AK Pen	<b>0.034</b>	0.013	<b>0.034</b>	0.019	0.005	0.031	0.079
NW GOA	<b>0.043</b>	0.009	<b>0.023</b>	0.020	0.000	0.018	0.075
Copper	<b>0.000</b>	0.000	<b>0.001</b>	0.003	0.000	0.000	0.007
NE GOA	<b>0.026</b>	0.004	<b>0.007</b>	0.012	0.000	0.000	0.043
Coast SE AK	<b>0.045</b>	0.004	<b>0.064</b>	0.025	0.023	0.061	0.120
BC	<b>0.228</b>	0.025	<b>0.216</b>	0.038	0.148	0.215	0.294
WA/OR/CA	<b>0.186</b>	0.022	<b>0.185</b>	0.035	0.122	0.184	0.260

Table 3. -- Regional SPAM and BAYES stock composition estimates for the 826 Chinook salmon samples from the bycatch of the 2010 Bering Sea groundfish trawl fishery. Standard deviations for the SPAM estimates were determined by the analysis of 1,000 bootstrapping resamplings of the mixture. The BAYES mean estimates are also provided with standard deviations (SD), 95% credible intervals, and the median estimate.

<b><u>Region</u></b>	<b><u>SPAM</u></b>	<b><u>SD</u></b>	<b><u>BAYES</u></b>	<b><u>SD</u></b>	<b><u>0.025</u></b>	<b><u>Median</u></b>	<b><u>97.5%</u></b>
Russia	<b>0.022</b>	0.003	<b>0.022</b>	0.005	0.013	0.022	0.034
Coast W AK	<b>0.433</b>	0.016	<b>0.416</b>	0.022	0.374	0.415	0.460
Mid Yukon	<b>0.096</b>	0.005	<b>0.112</b>	0.018	0.077	0.112	0.146
Up Yukon	<b>0.205</b>	0.010	<b>0.204</b>	0.017	0.171	0.203	0.238
N AK Pen	<b>0.126</b>	0.007	<b>0.141</b>	0.015	0.113	0.141	0.171
NW GOA	<b>0.017</b>	0.001	<b>0.006</b>	0.006	0.000	0.004	0.021
Copper	<b>0.001</b>	0.000	<b>0.000</b>	0.001	0.000	0.000	0.003
NE GOA	<b>0.002</b>	0.000	<b>0.000</b>	0.002	0.000	0.000	0.005
Coast SE AK	<b>0.009</b>	0.000	<b>0.009</b>	0.004	0.003	0.008	0.018
BC	<b>0.056</b>	0.003	<b>0.056</b>	0.008	0.041	0.056	0.073
WA/OR/CA	<b>0.034</b>	0.003	<b>0.035</b>	0.007	0.023	0.034	0.048

#### COMPARISON WITH PREVIOUS ESTIMATES

Stock compositions from the analysis of the 2010 “A” season Chinook salmon bycatch samples were in general agreement with the 2008 “A” season estimates. For example, most samples were from stocks originating from river systems directly flowing into the Bering Sea, although differences were noted for the Upper and Middle Yukon group (increased in 2010) and the Western Alaska and the Northern Alaska Peninsula groupings (decreased in 2010) (Fig. 5). With regard to the 2010 “B” season stock composition estimates, substantial differences were apparent when compared to previous years (Fig. 6). The largest differences were the decrease for Coastal Western Alaska stocks and the increase in British Columbia, West Coast U.S. and Coastal Southeast Alaska stocks in 2010. Since most of the Chinook salmon bycatch occurs during the spring “A” season, the sample sets available for the “B” season were smaller and

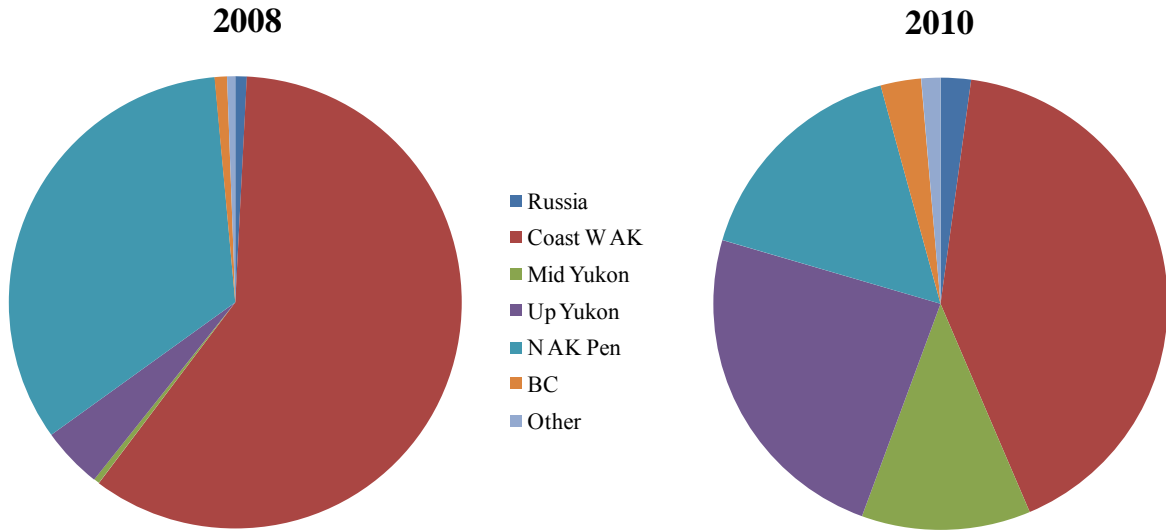


Figure 5. -- Comparison of “A” season genetic stock composition estimates for 2008 and 2010 based on available genetic samples from the Bering Sea Chinook salmon bycatch. The same genetic baseline and general regional groupings were used in all analyses. Other group consists of combined values from NWGOA, Copper, NE GOA, and Coast SE AK groupings.

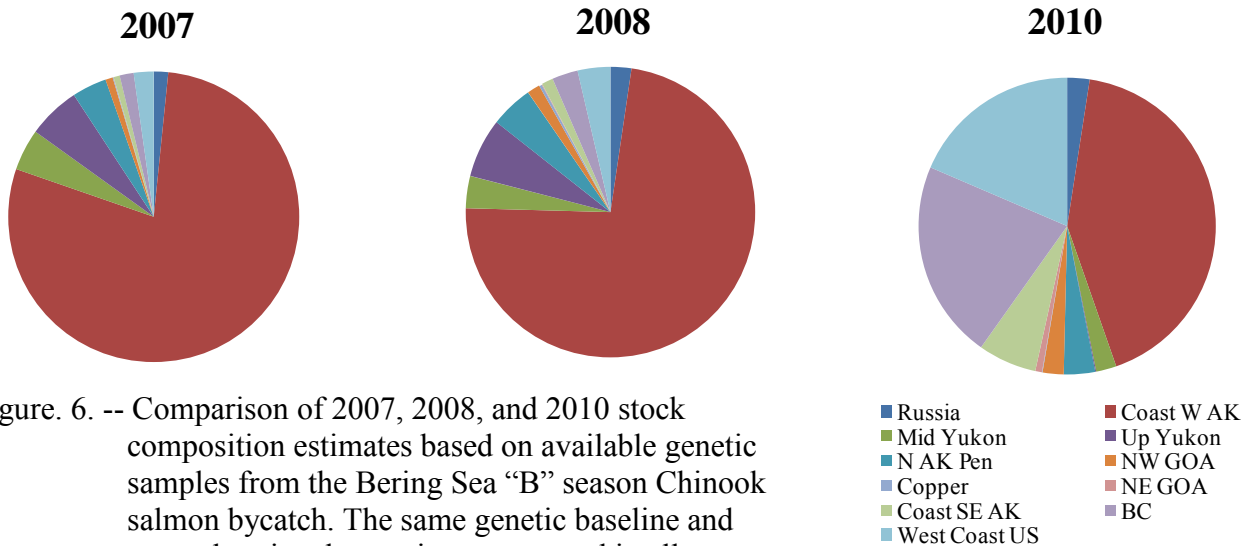


Figure 6. -- Comparison of 2007, 2008, and 2010 stock composition estimates based on available genetic samples from the Bering Sea “B” season Chinook salmon bycatch. The same genetic baseline and general regional groupings were used in all analyses.

therefore potentially subject to more stock variability implying that caution must be exercised in interpreting these results. When the stock compositions were analyzed for the entire year, Coastal Western Alaska and Northern Alaska Peninsula stock compositions trended downward

between 2008 and 2010, while the Yukon, British Columbia, and West Coast U.S. stock compositions slightly increased (Fig. 7). These changes may be the result of more representative sampling of the bycatch in 2010 or reflect true changes in the overall stock compositions.

## SUMMARY

Communities in western Alaska and elsewhere are dependent on Chinook salmon for subsistence and commercial purposes. Decreasing Chinook salmon returns to western Alaska rivers have caused hardships in these communities and led to the recent declaration of a fisheries disaster for Yukon River Chinook salmon by the U. S. Secretary of Commerce (Locke 2010). Salmon-dependent communities have expressed concern regarding the numbers of salmon caught as bycatch in the Bering Sea trawl fishery. The incidental harvest of Chinook salmon in the Bering Sea groundfish fishery averaged 46,453 salmon per year during 1992-2010, but

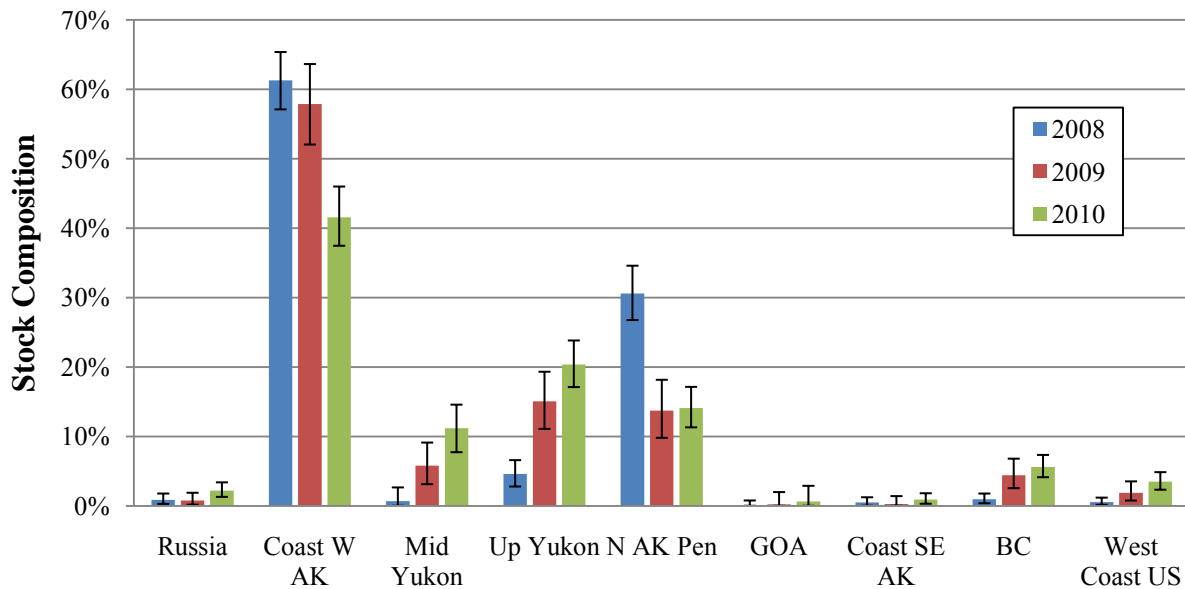


Figure 7. -- Comparison of yearly stock composition estimates (2008-2010) based on available genetic samples from the Bering Sea Chinook salmon bycatch. The same genetic baseline and general regional groupings were used in all analyses. GOA group consists of combined values for NWGOA, Copper, and NE GOA. BAYES 95% credible intervals are plotted for yearly estimates.

steadily increased to a peak of 129,567 in 2007. The Chinook salmon bycatch has abated in more recent years dropping to a total of 12,532 Chinook salmon in 2010 and a Chinook salmon bycatch management program was implemented in 2011 by the North Pacific Fishery Management Council to limit the amount of Chinook salmon taken in the pollock fishery and provide incentives to avoid Chinook salmon bycatch. Stock composition estimates of the Chinook salmon bycatch are needed for pollock and salmon fishery managers to understand whether the trawl fisheries may be impacting salmon returns. This report provides a stock composition analysis of genetic sample sets from the 2010 BSAI Chinook salmon bycatch. The results and limitations of this analysis are summarized below.

### Sampling Issues

The inherent spatial and temporal biases in the sample sets from previous years have been reduced in 2010 (Figs. 3-4). These past biases limited the application of the genetic sample stock composition estimates to the entire Chinook salmon bycatch, although the small sample size from the “B” season still causes concern. With regard to future improved sampling protocols, NMFS recently instituted a rule and notice of availability for Amendment 91 to the Fishery Management Plan for Groundfish of the BSAI Management Area (75 FR 14016, March 23, 2010). This rule will require that all salmon bycatch taken in the Bering Sea pollock fishery be sorted by species and counted to ensure compliance with the salmon bycatch caps for the pollock fishery. This may provide additional opportunity for observers to provide representative sampling of the salmon bycatch for genetic analysis, and improve the capability to characterize the origin of salmon taken as bycatch in the Bering Sea trawl fishery.

### Stock Composition Estimates

Overall, the majority (> 85%) of the genetic samples were collected from the 2010 “A” season, a time which accounted for over 75% of the total 2010 Chinook bycatch of the Bering Sea trawl fishery. Genetic stock composition analysis showed the majority of bycatch samples were from Alaskan stocks predominantly originating from river systems directly flowing into the Bering Sea. The Chinook salmon bycatch stock composition estimates for the 2010 “B” season differed from those of the 2010 “A” season, suggesting temporal differences in the available Chinook salmon stocks. This was especially apparent for Middle/Upper Yukon stocks (35.9% vs. 2.3%), and the British Columbia/West Coast U.S. stocks (3.4% vs. 40.2%).

### Application of These Estimates

The extent to which any salmon stock is impacted by the bycatch of the Bering Sea trawl fishery is dependent on many factors including (1) the overall size of the bycatch, (2) the age of the salmon caught in the bycatch, (3) the age of the returning salmon, and (4) the total escapement of the affected stocks taking into account lag time for maturity and returning to the river. As such, a higher contribution of a particular stock one year does not necessarily infer greater impact than a smaller estimate the next. Efforts to better understand these relationships and their impacts are the subject of additional work.

## ACKNOWLEDGMENTS

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## CITATIONS

- ADF&G (Alaska Department of Fish and Game). 2003. SPAM Version 3.7b: Statistics Program for Analyzing Mixtures. Alaska Department of Fish and Game, Commercial Fisheries Division, Gene Conservation Laboratory, Anchorage, Alaska.
- Gabriel, S., Ziaugra, L., and D. Tabbaa. 2009. SNP genotyping using the Sequenom MassARRAY iPLEX platform. *Current Protocols in Human Genetics Chapter 2*, Unit 2 12.
- Guyon, J. R., Guthrie, C. M., and H. Nguyen. 2010a. Genetic stock composition analysis of Chinook salmon bycatch samples from the 2008 Bering Sea pollock fishery. Report to the North Pacific Fishery Management Council. pp. 32.
- Guyon, J. R., Guthrie, C. M., and H. Nguyen. 2010b. Genetic Stock Composition Analysis of Chinook Salmon Bycatch Samples from the 2007 "B" Season and 2009 Bering Sea Trawl Fisheries, Report to the North Pacific Fisheries Management Council. pp. 32.
- Locke, G. 2010. Commerce Secretary Gary Locke announces "Fishery Failure" determination for Alaska Chinook salmon. In Commerce News release, January 15, 2010, U.S. Department of Commerce, Washington, DC.
- NMFS (National Marine Fisheries Service). 2009. Bering Sea Chinook salmon bycatch management - Volume 1, Final Environmental Impact Statement, National Oceanic and Atmospheric Administration, National Marine Fisheries Service, Alaska Regional Office, Juneau, AK.
- NMFS (National Marine Fisheries Service). 2011. BSAI Chinook salmon mortality estimates, 1991-present, National Oceanic and Atmospheric Administration, National Marine Fisheries Service, Alaska Regional Office, Juneau, AK.  
[http://www.fakr.noaa.gov/sustainablefisheries/inseason/chinook\\_salmon\\_mortality.pdf](http://www.fakr.noaa.gov/sustainablefisheries/inseason/chinook_salmon_mortality.pdf)
- Peakall, R., and P. E. Smouse. 2006. GenAEx 6: genetic analysis in Excel. Population genetic software for teaching and research. *Mol. Ecol. Notes* 6, 288-295.
- Pella, J., and H. J. Geiger. 2009. Sampling considerations for estimating geographic origins of Chinook salmon bycatch in the Bering Sea pollock fishery. Alaska Department of Fish and Game, Special Publication No. SP 09-08, 58 p.
- Pella, J., and M. Masuda. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. *Fish. Bull.*, U. S. 99, 151-167.
- Templin, W. D., Seeb, J. E., Jasper, J. R., Barclay, A. W., and L.W. Seeb. 2011. Genetic differentiation of Alaska Chinook salmon: the missing link for migratory studies. *Mol. Ecol. Res.* 11 (Suppl. 1): 226–246.



## APPENDIX

Appendix 1. -- Chinook salmon populations in the ADF&G SNP baseline with the regional designations used in the analyses of this report.

ADF&G number	Population name	Region number	Region
1	Bistraya River	1	Russia
2	Bolshaya River	1	Russia
3	Kamchatka River late	1	Russia
4	Pakhatcha River	1	Russia
8	Andreafsky River	2	Coast W AK
40	Aniak River	2	Coast W AK
9	Anvik River	2	Coast W AK
34	Arolik River	2	Coast W AK
54	Big Creek	2	Coast W AK
44	Cheeneetnuk River	2	Coast W AK
36	Eek River	2	Coast W AK
45	Gagaryah River	2	Coast W AK
41	George River	2	Coast W AK
10	Gisasa River	2	Coast W AK
7	Golsovia River	2	Coast W AK
33	Goodnews River	2	Coast W AK
35	Kanektok River	2	Coast W AK
38	Kisaralik River	2	Coast W AK
42	Kogruluk River	2	Coast W AK
37	Kwethluk River	2	Coast W AK
51	Mulchatna River	2	Coast W AK
53	Naknek River	2	Coast W AK
50	Nushagak River	2	Coast W AK
5	Pilgrim River	2	Coast W AK
48	Salmon River - Pitka Fork	2	Coast W AK
43	Stony River	2	Coast W AK
52	Stuyahok River	2	Coast W AK
46	Takotna River	2	Coast W AK
47	Tatlawiksuk River	2	Coast W AK
49	Togiak River	2	Coast W AK
11	Tozitna River	2	Coast W AK
39	Tuluksak River	2	Coast W AK
6	Unalakleet River	2	Coast W AK
17	Beaver Creek	3	Mid Yukon
18	Chandalar River	3	Mid Yukon
15	Chena River	3	Mid Yukon
12	Henshaw Creek	3	Mid Yukon
14	Kantishna River	3	Mid Yukon
16	Salcha River	3	Mid Yukon
19	Sheenjek River	3	Mid Yukon
13	South Fork Koyukuk River	3	Mid Yukon
27	Big Salmon River	4	Up Yukon
24	Blind River	4	Up Yukon
20	Chandindu River	4	Up Yukon
21	Klondike River	4	Up Yukon

ADF&G number	Population name	Region number	Region
26	Little Salmon River	4	Up Yukon
23	Mayo River	4	Up Yukon
30	Nisutlin River	4	Up Yukon
29	Nordenskiold River	4	Up Yukon
25	Pelly River	4	Up Yukon
22	Stewart River	4	Up Yukon
31	Takhini River	4	Up Yukon
28	Tatchun Creek	4	Up Yukon
32	Whitehorse Hatchery	4	Up Yukon
59	Black Hills Creek	5	N AK Pen
55	King Salmon River	5	N AK Pen
56	Meshik River	5	N AK Pen
57	Milky River	5	N AK Pen
58	Nelson River	5	N AK Pen
60	Steelhead Creek	5	N AK Pen
78	Anchor River	6	NW GOA
62	Ayakulik River	6	NW GOA
72	Benjamin Creek	6	NW GOA
61	Chignik River	6	NW GOA
69	Crescent Creek	6	NW GOA
76	Crooked Creek	6	NW GOA
65	Deception Creek	6	NW GOA
64	Deshka River	6	NW GOA
73	Funny River	6	NW GOA
70	Juneau Creek	6	NW GOA
63	Karluk River	6	NW GOA
77	Kasilof River mainstem	6	NW GOA
75	Kenai River mainstem	6	NW GOA
71	Killey Creek	6	NW GOA
79	Ninilchik River	6	NW GOA
67	Prairie Creek	6	NW GOA
74	Slikok Creek	6	NW GOA
68	Talachulitna River	6	NW GOA
66	Willow Creek	6	NW GOA
81	Bone Creek	7	Copper
82	E. Fork Chistochina River	7	Copper
85	Gulkana River	7	Copper
80	Indian River	7	Copper
87	Kiana Creek	7	Copper
88	Manker Creek	7	Copper
86	Mendeltna Creek	7	Copper
83	Otter Creek	7	Copper
84	Sinona Creek	7	Copper
90	Tebay River	7	Copper
89	Tonsina River	7	Copper
92	Big Boulder Creek	8	NE GOA
95	Kelsall River	8	NE GOA
96	King Salmon River	8	NE GOA
116	Klukshu River	8	NE GOA
91	Situk River	8	NE GOA
93	Tahini River	8	NE GOA

ADF&G number	Population name	Region number	Region
94	Tahini River - Pullen Creek Hatchery	8	NE GOA
111	Andrews Creek	9	Coast SE AK
110	Blossom River	9	Coast SE AK
102	Butler Creek	9	Coast SE AK
98	Chickamin River	9	Coast SE AK
99	Chickamin River - Little Port Walter	9	Coast SE AK
100	Chickamin River - Whitman Lake Hatchery	9	Coast SE AK
103	Clear Creek	9	Coast SE AK
104	Cripple Creek	9	Coast SE AK
112	Crystal Lake Hatchery	9	Coast SE AK
121	Dudidontu River	9	Coast SE AK
105	Genes Creek	9	Coast SE AK
114	Hidden Falls Hatchery	9	Coast SE AK
101	Humpy Creek	9	Coast SE AK
106	Kerr Creek	9	Coast SE AK
109	Keta River	9	Coast SE AK
97	King Creek	9	Coast SE AK
117	Kowatua River	9	Coast SE AK
118	Little Tatsemenie River	9	Coast SE AK
115	Macaulay Hatchery	9	Coast SE AK
113	Medvejie Hatchery	9	Coast SE AK
120	Nakina River	9	Coast SE AK
122	Tahltn River	9	Coast SE AK
108	Unuk River - Deer Mountain Hatchery	9	Coast SE AK
107	Unuk River - Little Port Walter	9	Coast SE AK
119	Upper Nahlin River	9	Coast SE AK
143	Big Qualicum River	10	BC
157	Birkenhead River spring	10	BC
128	Bulkley River	10	BC
148	Chilko River summer	10	BC
152	Clearwater River summer	10	BC
138	Conuma River	10	BC
124	Damdochax Creek	10	BC
130	Ecstall River	10	BC
158	Harrison River	10	BC
123	Kateen River	10	BC
125	Kincolith Creek	10	BC
133	Kitimat River	10	BC
135	Klinaklini River	10	BC
126	Kwinageese Creek	10	BC
153	Louis River spring	10	BC
154	Lower Adams River fall	10	BC
132	Lower Atnarko River	10	BC
131	Lower Kalum River	10	BC
155	Lower Thompson River fall	10	BC
139	Marble Creek	10	BC
156	Middle Shuswap River summer	10	BC
145	Morkill River summer	10	BC
136	Nanaimo River	10	BC
149	Nechako River summer	10	BC
140	Nitinat River	10	BC

ADF&G number	Population name	Region number	Region
127	Oweegee Creek	10	BC
137	Porteau Cove	10	BC
150	Quesnel River summer	10	BC
144	Quinsam River	10	BC
141	Robertson Creek	10	BC
146	Salmon River summer	10	BC
142	Sarita River	10	BC
151	Stuart River summer	10	BC
129	Sustut River	10	BC
147	Torpy River summer	10	BC
134	Wannock River	10	BC
168	Alsea River fall	11	West Coast US
166	Carson Hatchery spring	11	West Coast US
171	Eel River fall	11	West Coast US
160	Forks Creek fall	11	West Coast US
164	Hanford Reach	11	West Coast US
170	Klamath River	11	West Coast US
165	Lower Deschutes River fall	11	West Coast US
163	Lyons Ferry Hatchery summer/fall	11	West Coast US
159	Makah National Fish Hatchery fall	11	West Coast US
167	McKenzie River spring	11	West Coast US
172	Sacramento River winter	11	West Coast US
169	Siuslaw River fall	11	West Coast US
162	Soos Creek Hatchery fall	11	West Coast US
161	Upper Skagit River summer	11	West Coast US

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### AFSC-

- 231 SMITH, K. R., R. A. MCCONNAUGHEY, and C. E. ARMISTEAD. 2011. Benthic invertebrates of the Eastern Bering Sea: A synopsis of the life history and ecology of snails of the genus *Neptunea*., 58 p. NTIS number pending.
- 230 HIMES-CORNELL, A., C. PACKAGE, and A. DURLAND. 2011. Improving community profiles for the North Pacific fisheries, 85 p. NTIS number pending.
- 229 YANG, M-S. 2011. Diet of nineteen mesopelagic fishes in the Gulf of Alaska, 67 p. NTIS number pending.
- 228 LEW, D. K., and A. HIMES-CORNELL. 2011. A guide to designing, testing, and implementing Alaska Fisheries Science Center economic and social surveys, 43 p. NTIS No. PB2012100169.
- 227 LAUTH, R. R. 2011. Results of the 2010 eastern and northern Bering Sea continental shelf bottom trawl survey of groundfish and invertebrate fauna, 256 p. NTIS No. PB2012100168.
- 226 TESTA, J. W. (editor). 2011. Fur seal investigations, 2008-2009, 80 p. NTIS No. PB2012100205.
- 225 RARING, N. W., P. G. VON SZALAY, F. R. SHAW, M. E. WILKINS, and M. H. MARTIN. 2011. Data Report: 2001 Gulf of Alaska bottom trawl survey, 179 p. NTIS No. PB2011-111406.
- 224 HOFF, G. R., and L. L. BRITT. 2011. Results of the 2010 eastern Bering Sea upper continental slope survey of groundfish and invertebrate resources, 300 p. NTIS No. PB2011-111407.
- 223 ALLEN, B. M., and R. P. ANGLISS. 2011. Alaska marine mammal stock assessments, 2010, 292 p. NTIS No. PB2011-111461.
- 222 GRAY, A. K., W. T. MCCRANEY, C. T. MARVIN, C. M. KONDZELA, H. T. NGUYEN, and J. R. GUYON. 2011. Genetic stock composition analysis of chum salmon bycatch samples from the 2008 Bering Sea groundfish fisheries, 29 p. NTIS No. PB2011-110765.
- 221 GRAY, A. K., W. T. MCCRANEY, C. T. MARVIN, C. M. KONDZELA, H. T. NGUYEN, and J. R. GUYON. 2011. Genetic stock composition analysis of chum salmon bycatch samples from the 2007 Bering Sea groundfish fisheries, 29 p. NTIS No. PB2011-110764.
- 220 MARVIN, C. T., S. L. WILDES, C. M. KONDZELA, H. T. NGUYEN, and J. R. GUYON. 2011. Genetic stock composition analysis of chum salmon bycatch samples from the 2006 Bering Sea groundfish fisheries, 29 p. NTIS No. PB2011-108416.
- 219 JONES, D. T., A. De ROBERTIS, and N. J. WILLIAMSON. 2011. Statistical combination of multifrequency sounder-detected bottom lines reduces bottom integrations, 13 p. NTIS No. PB2011-108416.
- 218 LANDER, M. E., D. S. JOHNSON, J. T. STERLING, T. S. GELATT, and B. S. FADELY. 2011. Diving behaviors and movements of juvenile Steller sea lions (*Eumetopias jubatus*) captured in the central Aleutian Islands, April 2005, 41 p. NTIS No. PB2011108415.
- 217 LAZRUS, H. M., J. A. SEPEZ, R. G. FELTHOVEN, and J. C. LEE. 2011. Post-rationalization restructuring of commercial crew member opportunities in Bering Sea and Aleutian Island crab fisheries, 62 p. NTIS No. PB2011-107546.
- 216 CHILTON, E. A., C. E. ARMISTEAD, and R. J. FOY. 2011. The 2010 eastern Bering Sea continental shelf bottom trawl survey: Results for commercial crab species, 101 p. NTIS PB2011-108305.